```
        10                  30                  50
AAAGCACAGACTTCAGGTCTCCAAGGAGGATGGGTGGCTGCAGCACAAGAGGCAAGCGGC

                            M  G  G  C  S  T  R  G  K  R  P

        70                  90                  110
CGTCAGCCCTCAGTCTGCTGCTGCTGCTGCTGCTCTCGGGGATCGCAGCCTCTGCCCTCC

  S  A  L  S  L  L  L  L  L  L  L  S  G  I  A  A  S  A  L  P

       130                 150                 170
CCCTGGAGAGCGGTCCCACCGGCCAGGACAGTGTGCAGGATGCCACAGGCGGGAGGAGGA

  L  E  S  G  P  T  G  Q  D  S  V  Q  D  A  T  G  G  R  R  T

       190                 210                 230
CCGGCCTTCTGACTTTCCTTGCCTGGTGGCATGAGTGGGCTTCCCAAGACAGCTCCAGCA

  G  L  L  T  F  L  A  W  W  H  E  W  A  S  Q  D  S  S  S  T

       250                 270                 290
CCGCTTTCGAAGGGGGTACCCCGGAGCTGTCTAAGCGGCAGGAAAGACCACCCCTCCAGC

  A  F  E  G  G  T  P  E  L  S  K  R  Q  E  R  P  P  L  Q  Q

       310                 330                 350
AGCCCCCACACCGGGATAAAAAGCCCTGCAAGAACTTCTTCTGGAAAACCTTCTCCTCGT

  P  P  H  R  D  K  K  P  C  K  N  F  F  W  K  T  F  S  S  C

       370                 390                 410
GCAAGTAGCCCGAGCCTGACCGGAGCCTGACCGGCCACCCTGTGAATGCAGCCGTGGCCT

  K

       430
GAATAAAGAGTGTCAAGT
```

FIGURE 1

```
CST     10 RPSALSLLLLLLLSGIAASALPLESGPTGQDSVQDATGGRRTGLLTFLAW 59
           ...  .| ::| |:|:.:.: .    . |.|:..||| .  : . : .:
SST      7 QCALAALCIVLALGGVTGAPSDPRLRQFLQKSLAAATGKQELAKYFLAEL 56

CST     60 WHEWASQDSSSTAFEGGTPELSKRQERPPLQQ.....PPHRDKKPCK 101
           : | .  :... . |: ... .. : | .||.       :|:  | .||
SST     57 LSEPNQTENDALEPEDLPQAAEQDEMRLELQRSANSNPAMAPRERKAGCK 106

CST    102 NFFWKTFSSCK
           |||||||.||.
SST    107 NFFWKTFTSC
```

FIGURE 2

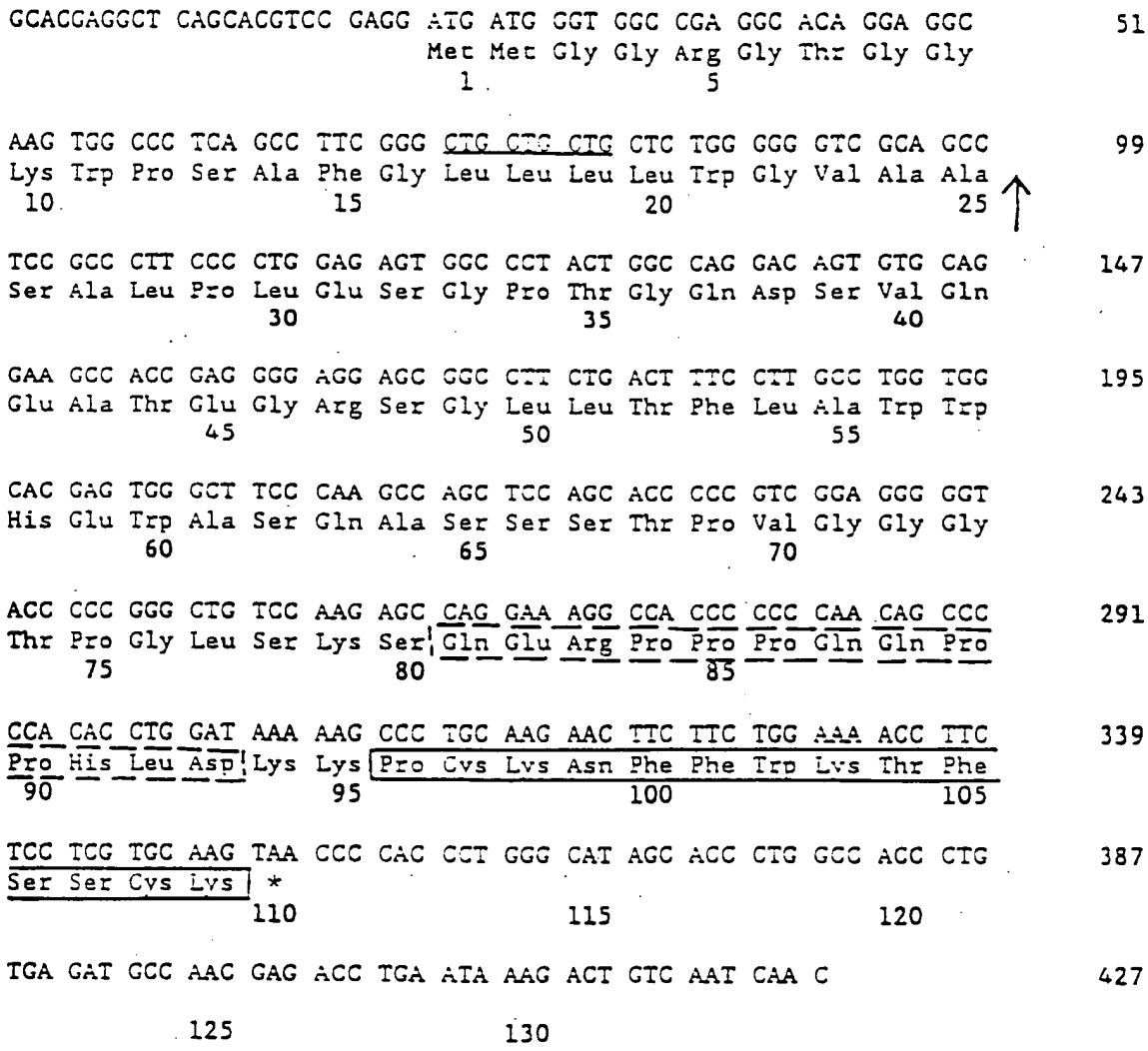

GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC 51
Met Met Gly Gly Arg Gly Thr Gly Gly
1 5
AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC 99
Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Trp Gly Val Ala Ala
10 15 20 25
TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG 147
Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
30 35 40
GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG 195
Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
45 50 55
CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT 243
His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly
60 65 70
ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC 291
Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro
75 80 85
CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC 339
Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe
90 95 100 105
TCC TCG TGC AAG TAA CCC CAC CCT GGG CAT AGC ACC CTG GCC ACC CTG 387
Ser Ser Cys Lys *
110 115 120
TGA GAT GCC AAC GAG ACC TGA ATA AAG ACT GTC AAT CAA C 427
125 130

FIGURE 3

```
MOUSE CST    .......... ...GCACGAG GCTCAGCACG TCCGAGGATG ATGGGTGGCC
RAT CT       .......... .AAAGCACAG ACTTCAGGTC TCCAAGGAGG ATGGGTGGCT
HUMAN CST    GGCACGAGGC CAAACATTGA TTTCAGGGCT GCCAGGAAGG AAGAGCAGCA

MOUSE CST    GAGGCACAGG AGGCAAGTGG CCCTCAG... .......... .....CCTTC
RAT CST      GCAGCACAAG AGGCAAGCGG CCGTCAG... .......... .....CCCTC
HUMAN CST    GCAGGGTGGG AGAGAAGCTC CAGTCAGCCC ACAAGATGCC ATTGTCCCCC

MOUSE CST    GG........ .GCTGCTGCT GCTCTGGGGG GTCGCAGCCT CCGCCCTTCC
RAT CST      AGTCTGCTGC TGCTGCTGCT GCTCTCGGGG ATCGCAGCCT CTGCCCTCCC
HUMAN CST    GGCCTCCTGC TGCTGCTGCT CTCCGGGGCC ACGGCCACCG CTGCCCTGCC

MOUSE CST    CCTGGAGAGT GGCCCTACTG GCCAGGACAG ......TGTG CAGGAAGCCA
RAT CST      CCTGGAGAGC GGTCCCACCG GCCAGGACAG ......TGTG CAGGATGCCA
HUMAN CST    CCTGGAGGGT GGCCCCACCG GCCGAGACAG CGAGCATATG CAGGAAGCGG

MOUSE CST    C...CGAGGG GAGGAGCGGC CTTCTGACTT TCCTTGCCTG GTGGCACGAG
RAT CST      CAGGCGGGAG GAGGACCGGC CTTCTGACTT TCCTTGCCTG GTGGCATGAG
HUMAN CST    CAGGAATAAG GAAAAGCAGC CTCCTGACTT TCCTCGCTTG GTGGTTTGAG

MOUSE CST    TGGGCTTCCC AAGCCAGCTC CAGCACCCCC GTCGGAGGGG GTACCCCCGG
RAT CST      TGGGCTTCCC AAGACAGCTC CAGCACCGCT TTCGAAGGGG GTACCCCGGA
HUMAN CST    TGGACCTCCC AGGCCAGTGC CGGGCCCCTC ATAGGAGAGG AAGCCCGGGA

MOUSE CST    GCTGTCCAAG AGCCAGGAAA GGCCACCCCC CCAACAGCCC CCACACCTGG
RAT CST      GCTGTCTAAG CGGCAGGAAA GACCACCCCT CCAGCAGCCC CCACACCGGG
HUMAN CST    GGTGGCCAGG CGGCAGGAAG GCGCACCCCC CCAGCAATCC GCGCGCCGGG

MOUSE CST    ATAAAAAGCC CTGCAAGAAC TTCTTCTGGA AAACCTTCTC CTCGTGCAAG
RAT CST      ATAAAAAGCC CTGCAAGAAC TTCTTCTGGA AAACCTTCTC CTCGTGCAAG
HUMAN CST    ACAGAATGCC CTGCAGGAAC TTCTTCTGGA AGACCTTCTC CTCCTGCAAA

MOUSE CST    TAACCCCACC CTGGGCATAG CACCCTGGCC ACCCTGTGAG ATGCCAACGA
RAT CST      TAGCCCGAGC CTGACCGGAG CCTGACCGGC CACCCTGTGA ATGCAGCCGT
HUMAN CST    TAAAACCTCA CCCATGAATG C......... .TCACGCAAG TGTAATGACA

MOUSE CST    GACCTGAATA AAGACTGTCA ATCAAC.... .......... ..........
RAT CST      GGCCTGAATA AAGAGTGTCA AGT....... .......... ..........
HUMAN CST    GACCTGAATA AAATGTATTA AGCAGCAGTG ATCTTTCCTC TCCTCCTTCC
                        *
MOUSE CST    .......... .......... .......... .......... ..........
RAT CST      .......... .......... .......... .......... ..........
HUMAN CST    CAAGTCATTG AAAAGTGTTT GTTATTTAAA TTCCAATAAT GCCCAATACT

MOUSE CST    .......... .......... .......... .......... ..........
RAT CST      .......... .......... .......... .......... ..........
HUMAN CST    GACGTGTCTT GAGTAATTTG GAACCCAAAA GTGAAGATCT TTGATAAAGA

MOUSE CST    .......... .......... .......... .......... ..........
RAT CST      .......... .......... .......... .......... ..........
HUMAN CST    TTTTTTTTGT GGTTCGACTG GACTGTGCTG AGTGCGGGCA CTGGGCTTTT

MOUSE CST    .......... .......... .......... .......... ..........
RAT CST      .......... .......... .......... .......... ..........
HUMAN CST    CTTCTGATGT TCATTATGGT GCTGGGAAGC TCTGTCTTTG ATTTAAAATA
                                                                  *
MOUSE CST    .......... ..........
RAT CST      .......... ..........
HUMAN CST    AAATAGCTAA AGGCTACAC
```

FIGURE 3a

```
           1                                                    50
RAT CST    .MGGCSTRGK RPSALSLLLL LLLSGIAASA LPLESGPTGQ DS..VQDATG
MOUSE CST  MMGGRGTGGK WPSAFGLLLL W...GVAASA LPLESGPTGQ DS..VQEATE
HUMAN CST  .......... MPLSPGLLLL LLSGATATAA LPLEGGPTGR DSEHMQEAAG
Consensus  ---------- -P----LLLL ------A--A LPLE-GPTG- DS---Q-A--

           51                                                   100
RAT CST    GRRTGLLTFL AWWHEWASQD SSSTAFEGGT PELSKRQERP PLQQPPHRDK
MOUSE CST  G.RSGLLTFL AWWHEWASQA SSSTPVGGGT PGLSKSQERP PPQQPPHLDK
HUMAN CST  IRKSSLLTFL AWWFEWTSQA SAGPLIGEEA REVARRQEGA PPQQSARRDR
Consensus  -----LLTFL AWW-EW-SQ- S--------- ------QE-- P-QQ----D-

           101          116
RAT CST    KPCKNFFWKT FSSCK
MOUSE CST  KPCKNFFWKT FSSCK
HUMAN CST  MPCRNFFWKT FSSCK
Consensus  -PC-NFFWKT FSSCK
```

FIGURE 3b

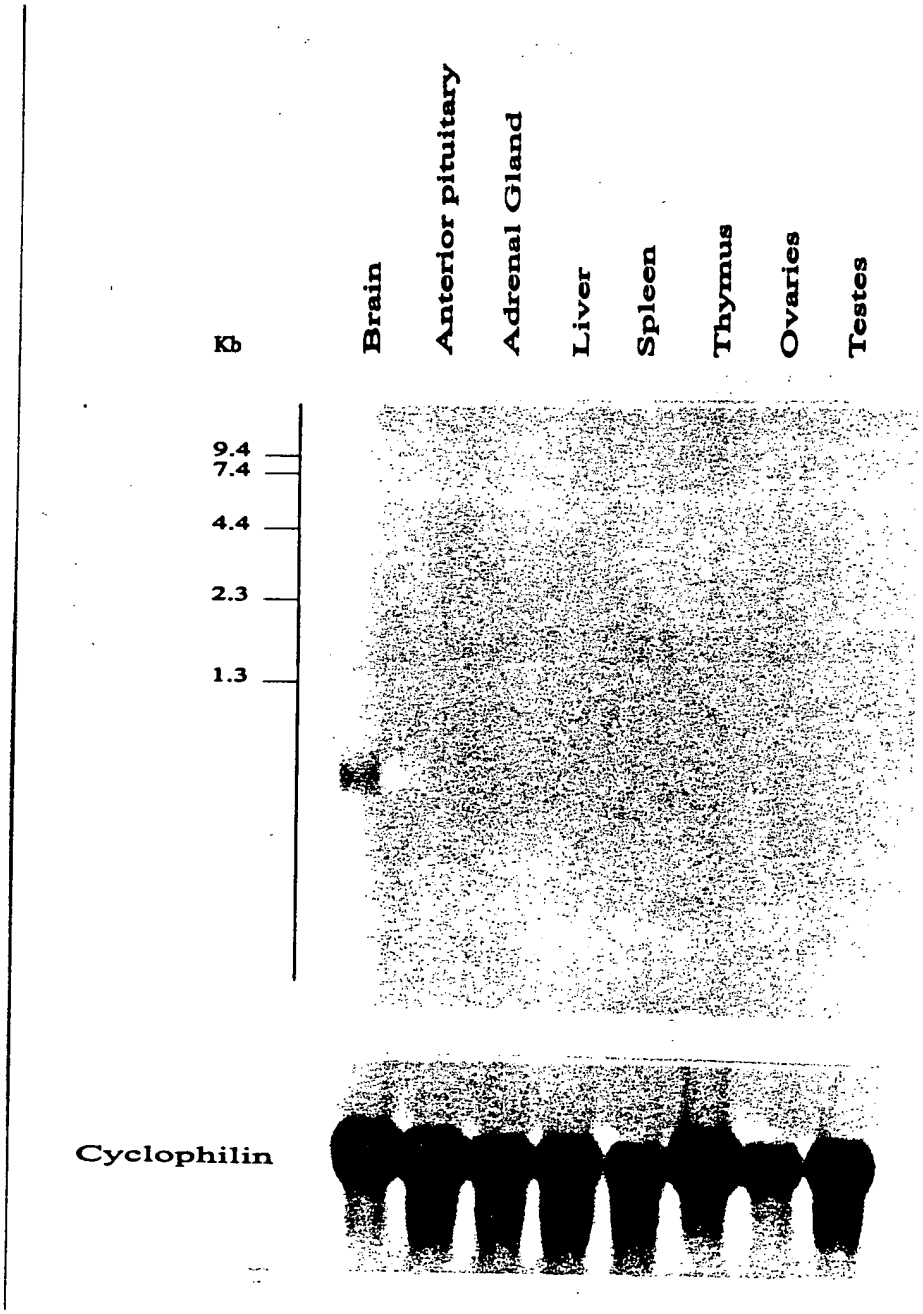
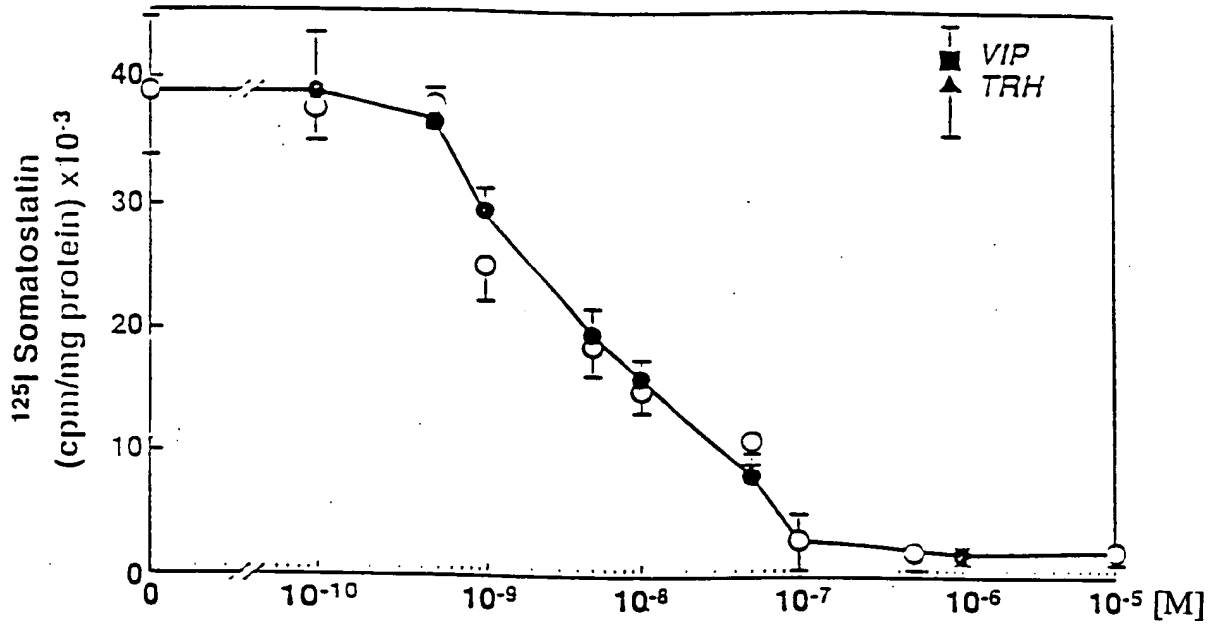
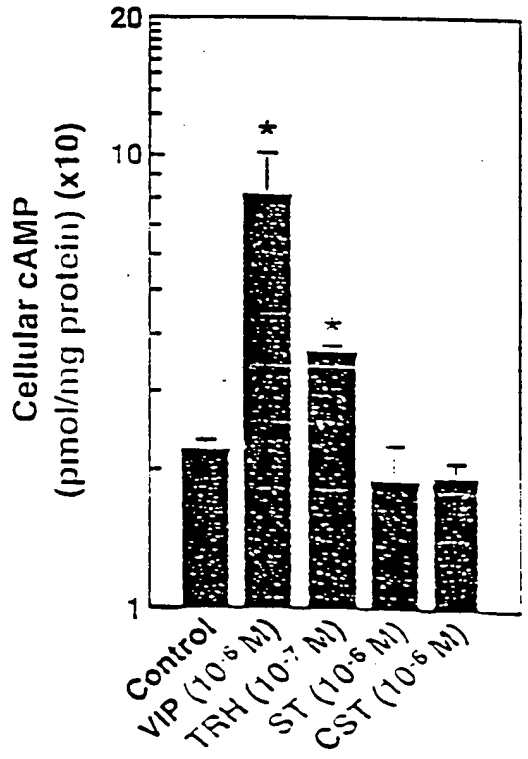

Kb
Brain
Anterior pituitary
Adrenal Gland
Liver
Spleen
Thymus
Ovaries
Testes
9.4
7.4
4.4
2.3
1.3
Cyclophilin

FIGURE 4

5A



5B



5C

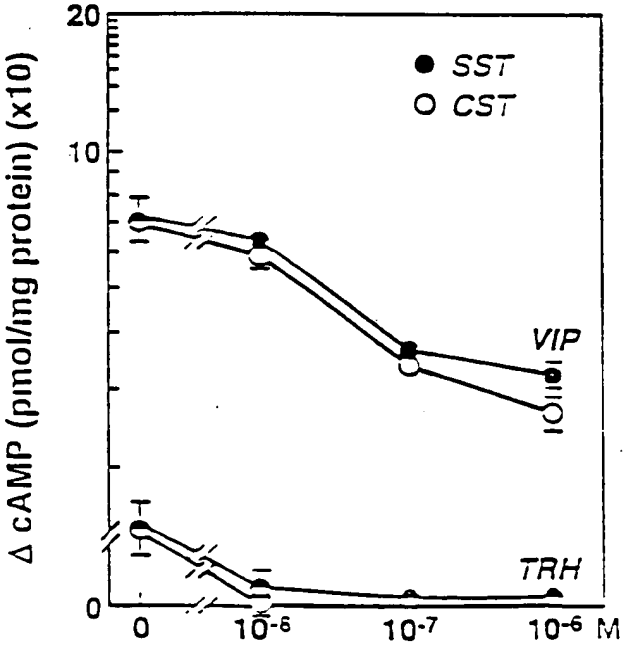
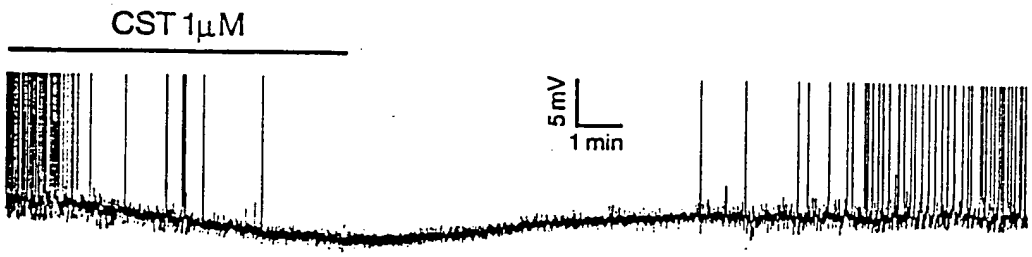
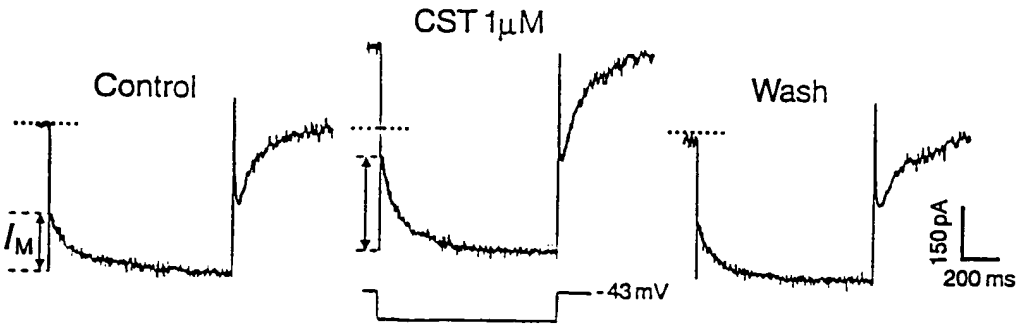


FIGURE 5

6A



6B



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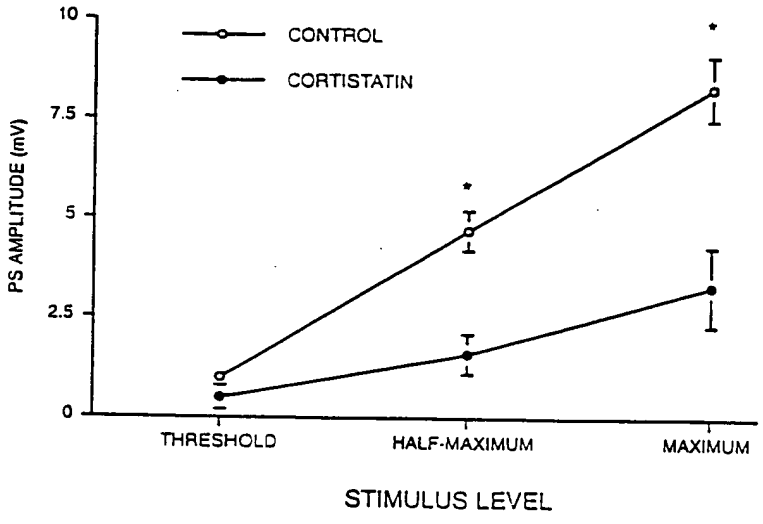
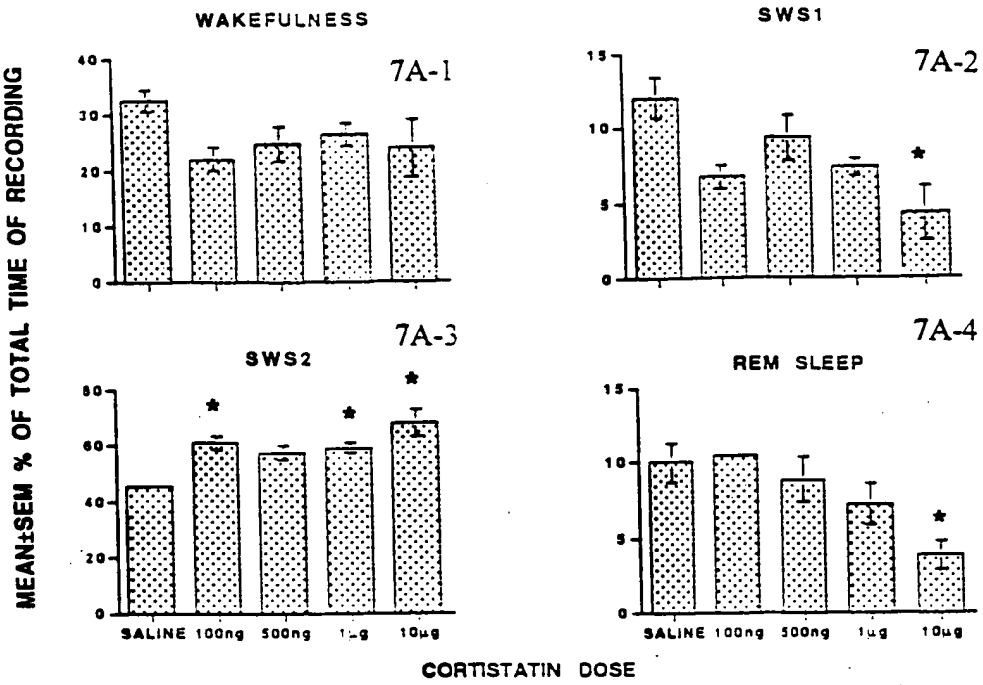
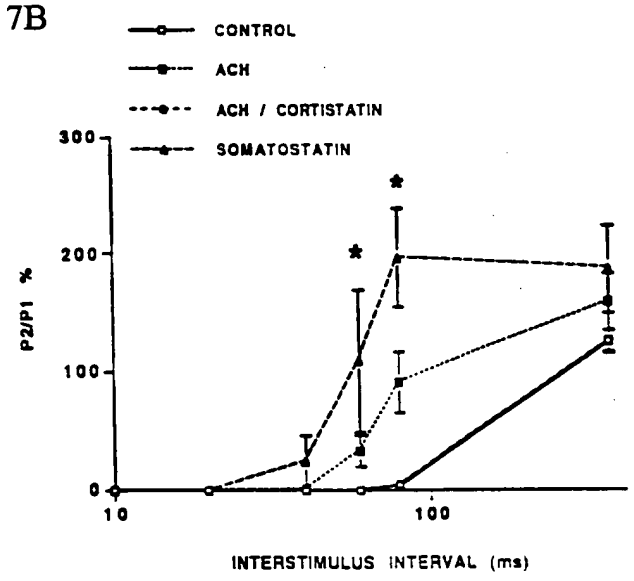


FIGURE 6

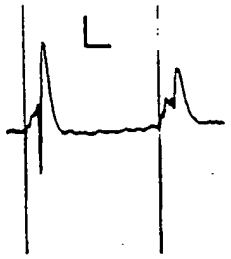
7A



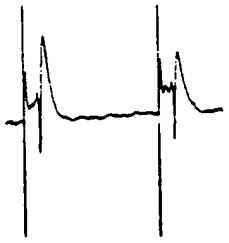
7B



7C

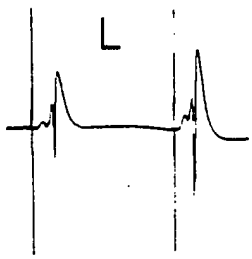


7D



7E

7F



7G

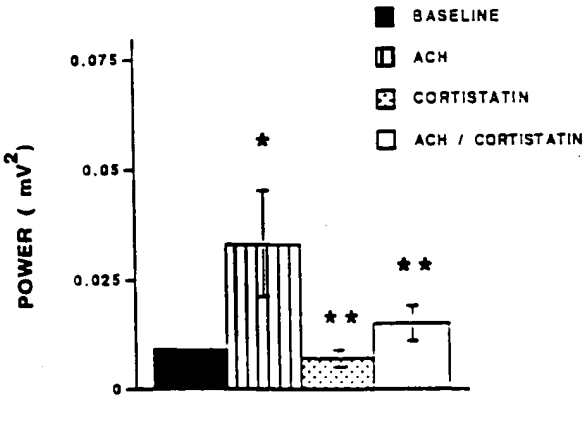


FIGURE 7